Increased respiratory morbidity associated with exposure to a mature volcanic plume from a large Icelandic fissure eruption

Supplementary Information

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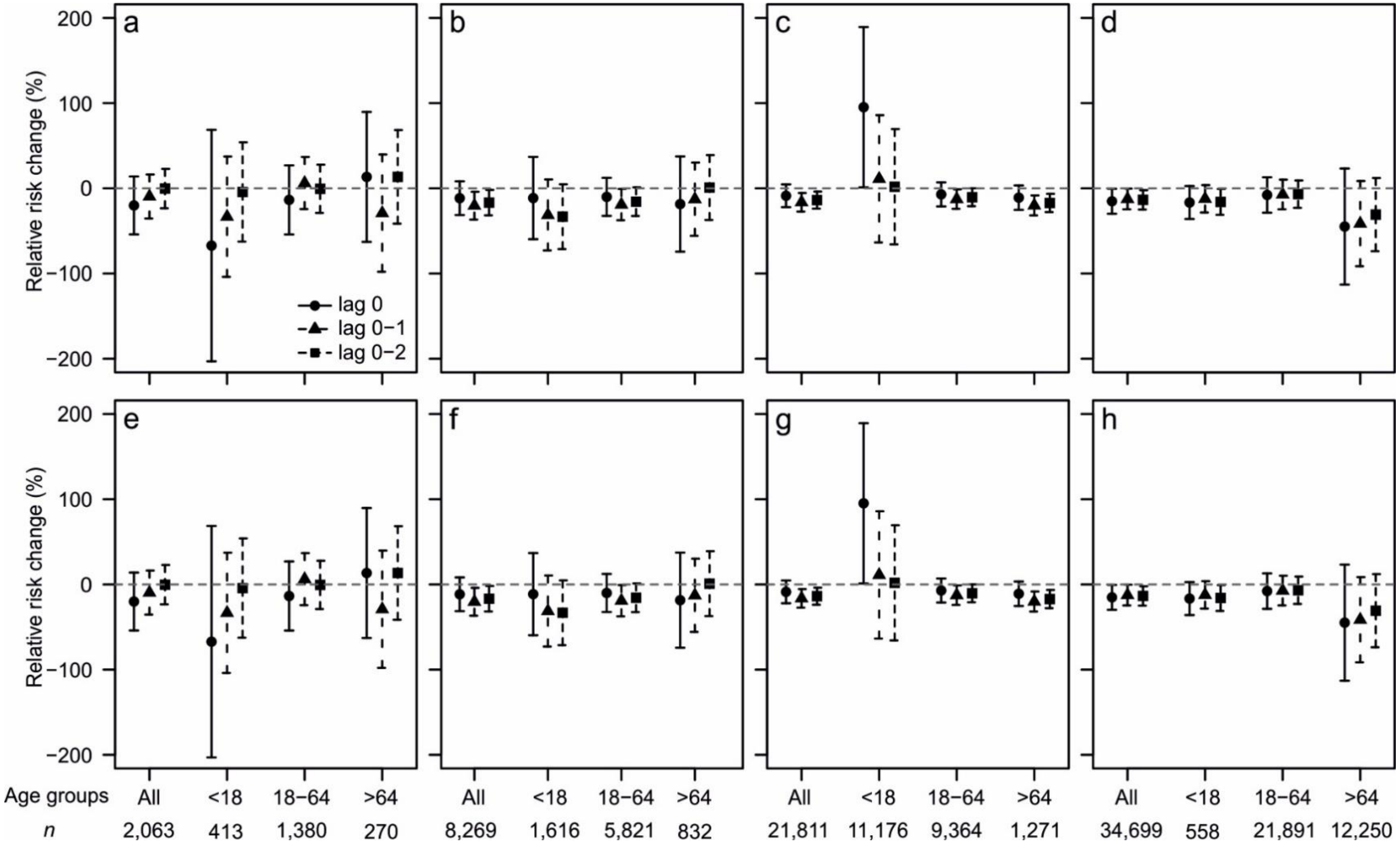
This file contains

Supplementary Figures 1-3

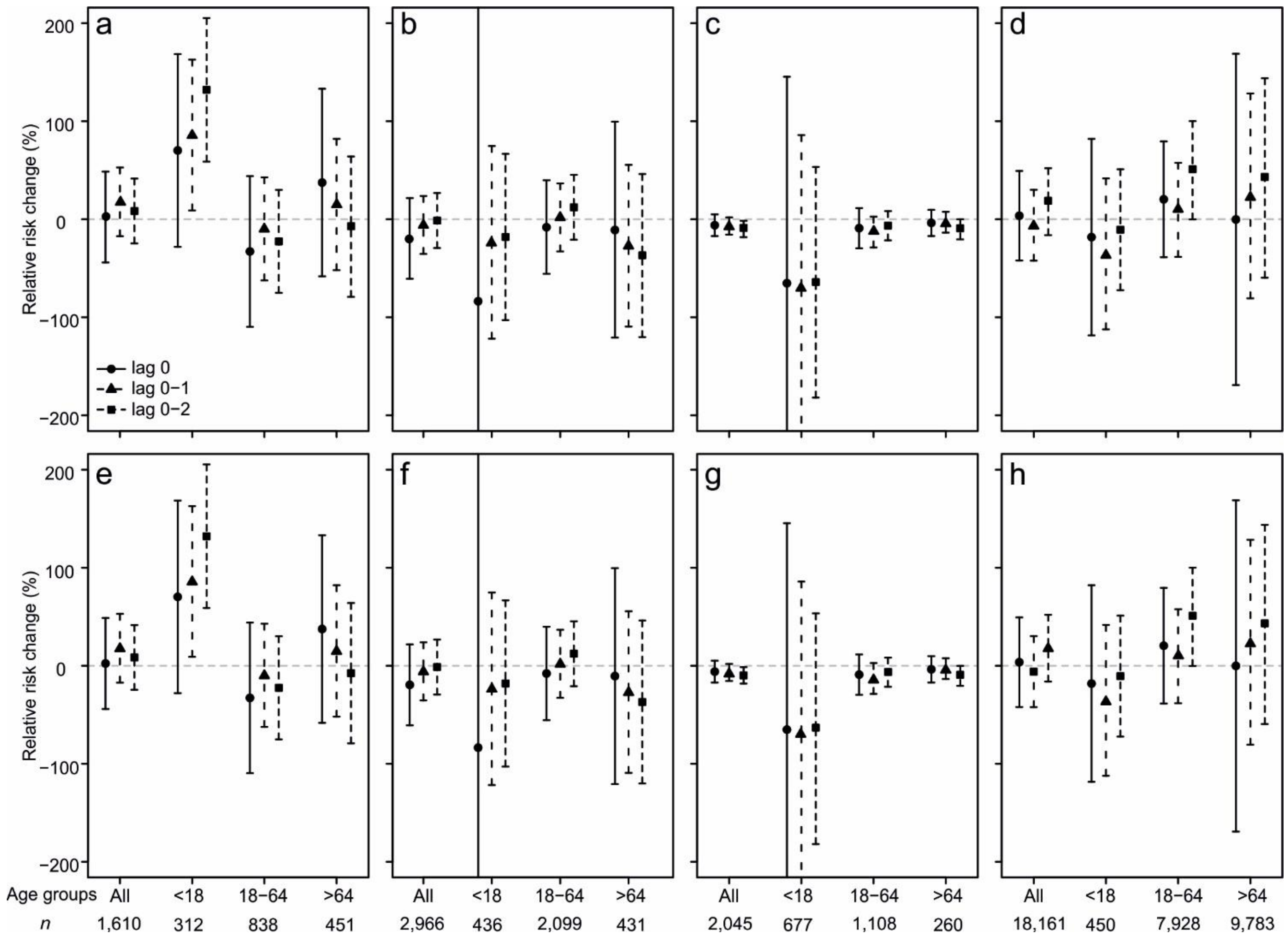
Supplementary Methods

Supplementary Figures

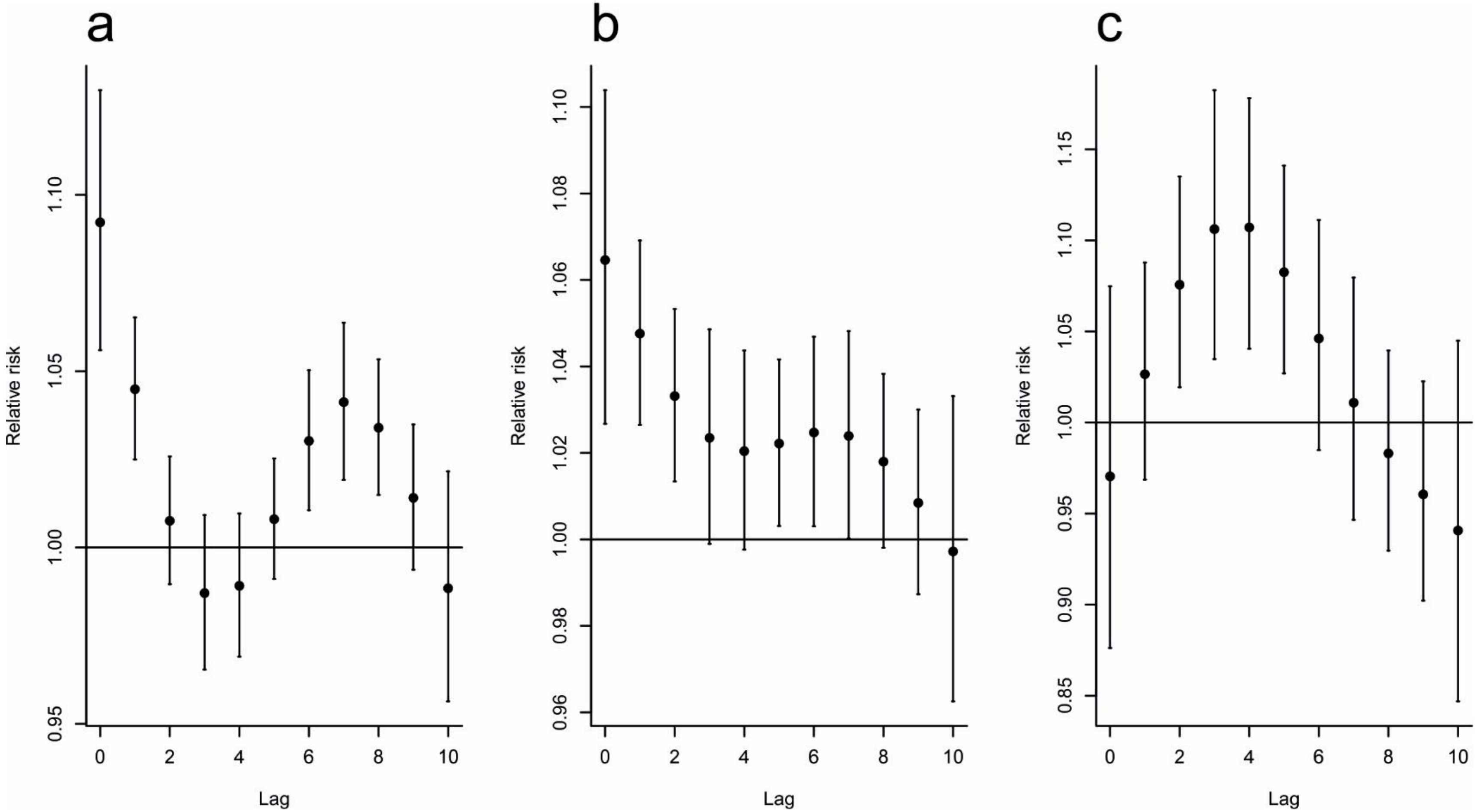
Supplementary Figure 1 Associations between exposure to mature plume and PCMD visits for non-respiratory diagnosis categories (ICD codes and *n* of individuals in brackets). (a-d) show unadjusted results for mature plume exposure. (e-h) show results adjusted for SO_2, an indicator of the primitive plume. (a, e) Nausea and vomiting (R11, *n* = 2,063 individuals); (b, f) Headaches (R51, *n* = 8,269 individuals); (c, g) Circulatory system disease (I, *n* = 21,811 individuals); (d, h) Eye irritation (H10-H11, *n* = 34,699 individuals). Results are reported as percent change in RR with error bars showing the 95% confidence intervals. Results are shown for different age groups (all age groups combined; < 18 years; 18-64 years; > 64 years) for several lag combinations; *n* of individuals in each age group is shown on the x-axis.



Supplementary Figure 2 Associations between exposure to mature plume and HED visits for non-respiratory diagnosis categories (ICD codes and *n* of individuals in brackets). (a-d) show unadjusted results for mature plume exposure. (e-h) show results adjusted for SO_2, an indicator of the primitive plume. (a, e) Nausea and vomiting (R11, *n* = 1,610 individuals); (b, f) Headaches (R51, *n* = 2,966 individuals); (c, g) Circulatory system disease (I, *n* = 2,045 individuals); (d, h) Eye irritation (H10-H11, *n* = 18,161 individuals). Results are reported as percent change in RR with error bars showing the 95% confidence intervals. Results are shown for different age groups (all age groups combined; < 18 years; 18-64 years; > 64 years) for several lag combinations; *n* of individuals in each age group is shown on the x-axis.



Supplementary Figure 3 Lag-associations for exposure to mature plume and health outcomes the following day, modelled with splines. (a) Association with AMD, *n* = 48,014 individuals; (b) Association with PCMD visits for respiratory diagnoses, *n* = 110,809 individuals; (c) Association with HED for respiratory diagnoses, *n* = 20,725 individuals. Results are reported as change in RR with error bars showing the 95% confidence intervals.



Supplementary Methods

R code model examples

1. Unadjusted results (Figure 2a-c, Figure 4, Supplementary Figure 1a-d, Supplementary Figure 2a-d).

model <- gam(outcome ~ Mature_plume_indicator + as.factor(day_of_week) + odd_holidays + s(day of time series, k=10) + s(day of year, bs="cc") , family=poisson(), data=data)

Where *outcome* is the number of visits or dispensings for the different health outcomes, outcome_lag1 is the outcome at lag 1 (to diminish autocorrelation).

2. SO_2-adjusted results (Figure 2d-f, Supplementary Figure 1e-h, Supplementary Figure 2e-h)

model <- gam(outcome ~ Mature_plume_indicator + SO_2 + as.factor(day_of_week) + odd_holidays + s(day of time series, k=10) + s(day of year, bs="cc") , family=poisson(), data=data)

Where the SO_2 term has the same lag as the mature plume exposure.

For anti-asthma medication dispensing, we use the quasipoisson distribution (*family=quasipoisson ()*)and for PCMD and HED, we use the poisson distribution (*family=poisson()*).

3. Lag-association model comparing mature plume and SO_2 (Figure 3 and Supplementary Figure 3)

#first, a cross basis was created for the mature plume, with lags up to 5 or 10 days, with a linear structure across the variable values and polynomial structure with 4 degrees of freedom for the lag structure.

```
cb.plume<- crossbasis(data_ph$mature plume,lag=5
                    , argvar=list(fun="lin")
                    , arglag=(list(fun="poly", degree=4)))
```

#Then, a cross basis was created for SO_2, with lags up to 5 or 10 days, with a threshold structure for variable values and polynomial structure with 4 degrees of freedom for the lag structure.

```
cb.so2<- crossbasis(data_ph$so2,lag=10
                    , argvar=list("thr",thr.value=c(5))
                   , arglag=(list(fun="poly", degree=4)))
```

#A model is constructed

```
 model <- gam(outcome ~cb.plume + cb.so2
              +as.factor(day_of_week)  +s(nday, k=4)
               +oddho+ s(doy3, bs="cc"), data=data, family=quasipoisson())
```

And the outcome of this model is used to predict based

a) for the mature plume crossbasis

```
pred.hgJ12<- crosspred(cb.plume,model, at=0:1)
```

b) the SO_2 crossbasis to the value 125.

```
pred.hgJ12_so2 <- crosspred(cb.so2,model,at=0:125)
```

And then extracted and plotted using “plot”.